



Revised March 29, 2004- 39754-0611 US.txt

# SEQUENCE LISTING

<110> WALKER, Ameae M.

<120> PROLACTIN ANTAGONISTS AND USES THEREOF

<130> 39754-0611-1CP1CP

<140> US 09/065,330

<141> 1998-04-23

<150> PCT/US97/01435

<151> 1997-01-30

<150> US 08/594,809

<151> 1996-01-31

<160> 6

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (622)...(624)

<223> This is the codon for the substituted amino acids  
of the mutated sequence.

<400> 1

aacatgaaca	tcaaaggatc	gccatggaaa	gggtccctcc	tgctgctgct	ggtgtcaaac	60
ctgctgctgt	gccagagcgt	ggcccccttg	cccattctgtc	ccggcggggc	tgcccgatgc	120
caggtgaccc	ttcgagacct	gtttgaccgc	gccgtcgtcc	tgtcccacta	catccataac	180
ctctcctcag	aaatgttcag	cgaattcgat	aaacgggtata	cccatggccg	ggggttcatt	240
accaaggcca	tcaacagctg	ccacacttct	tcccttgcca	ccccgaaga	caaggagcaa	300
gccaacaga	tgaatcaaaa	agactttctg	agcctgatag	tcagcatatt	gcgatcctgg	360
aatgagcctc	tgtatcatct	ggtcacggaa	gtacgtggta	tgcaagaagc	cccggaggct	420
atcctatcca	aagctgtaga	gattgaggag	caaaccaaac	ggcttctaga	gggcatggag	480
ctgatatgta	gccagggtta	tcctgaaacc	aaagaaaatg	agatctaccc	tgtctggtcg	540
ggacttccat	ccctgcagat	ggctgatgaa	gagtctcgcc	tttctgctta	ttataacctg	600
ctccactgcc	tacgcaggga	tnnncataaa	atcgacaatt	atctcaagct	cctgaagtgc	660
cgaatcatcc	acaacaacaa	ctgctaagcc	cacatccatt	tcatctattt	ctgagaagggt	720
ccttaatgat	ccgttccatt	gcaagcttct	tttagttgta	tctcttttga	atccatgctt	780
gggtgtaaca	ggtctcctct	taaaaaataa	aaactgactc	gtagagaca	tc	832

<210> 2

<211> 228

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 208

<223> Site mutated amino acid residue where the normal  
codon coding for serine is modified preferably to encode  
for aspartate or glutamate, most preferably  
aspartate.

<400> 2

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Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu Leu
 1      5      10      15
Leu Val Ser Asn Leu Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile
      20      25      30
Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe
      35      40      45
Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu
      50      55      60
Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile
      65      70      75      80
Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu
      85      90      95
Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu
      100      105      110
Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val
      115      120      125
Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys
      130      135      140
Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu
      145      150      155      160
Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr
      165      170      175
Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser
      180      185      190
Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa
      195      200      205
His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His
      210      215      220
Asn Asn Asn Cys
225

```

<210> 3

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<400> 3

gcagggatga ccacaaggtt gac

23

<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<220>

<221> variation

<222> 12

<223> This is a nucleic acid residue that can be replaced for nucleic acid substitutes.

<400> 4

cgcaaggat gnacacaagg ttga

24

<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<220>

<221> variation

<222> 12

<223> This is a nucleic acid residue that can be replaced for nucleic acid substitutes.

<400> 5

acgcagggat gnkataaaat cg

22

<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> This sequence is a primer.

<400> 6

cgtggccccc atatgttgcc catctg

26